Amendments to the Claims:

Listing of Claims:

1. (Original) A method for modulating the levels of a metabolic or biosynthetic product in a plant, including introducing a product into a plant, said method comprising introducing a genetic sequence encoding the product or a precursor to said product, or encoding an enzyme for the biosynthesis or metabolism of the product or a precursor of said product or a genetic sequence which alters the level of expression of a gene encoding a product or an enzyme capable of acting on the product, into a cell or group of cells of said plant, wherein the plant is a member of the family *Saccharum* genus, and wherein said metabolic or biosynthetic product comprises a polyhydroxyalanoate, a mixture of polyhydroxyalanoates or a precursor thereof.

2. (Original) The method of Claim 1 herein the member of the *Saccharum* genus is sugarcane.

3. (Currently Amended) The method of Claim 1 wherein the polyhydroxyalkanoate is polyhydroxybutryate.

4. (Original) The method of Claim 1 wherein the genetic sequence comprises one or more genetic sequences selected from the list comprising:-

(i) a nucleotide sequence encoding a phaA or homolog thereof;

(ii) a nucleotide sequence encoding phaB or homolog thereof;

(iii) a nucleotide sequence encoding phaC or homolog thereof;

(iv) a nucleotide sequence encoding phaC1 or homolog thereof;

(v) a nucleotide sequence encoding phaG or homolog thereof;

(vi) a nucleotide sequence encoding phaJ or homolog thereof

(vii) SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a complementary form thereof under low stringency conditions;

(viii) SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a complementary form thereof under low stringency conditions;

(ix) SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a complementary form thereof under low stringency conditions;

(x) SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a complementary form thereof under low stringency conditions;

(xi) SEQ ID NO:28 or SEQ ID NO:30 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:28 or SEQ ID NO:30 or a complementary form thereof under low stringency conditions;

(xii) SEQ ID NO:31 or SEQ ID NO:33 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:31 or SEQ ID NO:33 or a complementary form thereof under low stringency conditions.

5. (Original) A genetically modified *Saccharum* sp. cell comprising a genetic sequence encoding a metabolic or biosynthetic product or a precursor to said product, or encoding an enzyme for the biosynthesis or metabolism of the product or a precursor of said product or a genetic sequence which alters the level of expression of a gene encoding a product or an enzyme capable of acting on the product wherein said metabolic or biosynthetic product comprises a polyhydroxyalanoate, a mixture of polyhydroxyalanoates or a precursor thereof.

6. (Original) The *Saccharum* sp. cell of Claim 5, wherein said *Saccharum* sp. is sugarcane.

7. (Currently Amended) The *Saccharum* sp. cell of Claim 5 ~~or 6~~, wherein the polyhydroxyalkanoate is polyhydroxybutryate.

8. (Currently Amended) The genetically modified *Saccharum* sp. cell of ~~any one of~~ Claims 5 ~~to 7~~, wherein said genetically modified cell comprises one or more of the genetic sequences selected from the list comprising:-

(i) a nucleotide sequence encoding a phaA or homolog thereof;

(ii) a nucleotide sequence encoding phaB or homolog thereof;

(iii) a nucleotide sequence encoding phaC or homolog thereof;

(iv) a nucleotide sequence encoding phaC1 or homolog thereof;

(v) a nucleotide sequence encoding phaG or homolog thereof;

(vi) a nucleotide sequence encoding phaJ or homolog thereof

(vii) SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a complementary form thereof under low stringency conditions;

(viii) SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a complementary form thereof under low stringency conditions;

(ix) SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a complementary form thereof under low stringency conditions;

(x) SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a complementary form thereof under low stringency conditions;

(xi) SEQ ID NO:28 or SEQ ID NO:30 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:28 or SEQ ID NO:30 or a complementary form thereof under low stringency conditions;

(xii) SEQ ID NO:31 or SEQ ID NO:33 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:31 or SEQ ID NO:33 or a complementary form thereof under low stringency conditions.

~~recited in Claim 4~~.

9. (Currently Amended) A genetically modified *Saccharum* sp. plant comprising one or more cells ~~of any one of~~ claims 5 ~~to 8~~.

10. (Original) Seeds or other reproductive material or propagation material from the plant of Claim 9.

11. (Currently Amended) A polyhydroxyalkanoate polymer or mixture of polyalkanoate polymers produced according to the method of ~~any one of~~ Claims 1 ~~to 4~~.

12. (Currently Amended) A plant based bioreactor system used for the production of a metabolic or biosynthetic product, said bioreactor comprising one or more genetically modified cells of ~~any one of~~ Claims 5 ~~to 8~~ or one or more *Saccharum* sp. plants of ~~Claim 9~~comprising said cells.